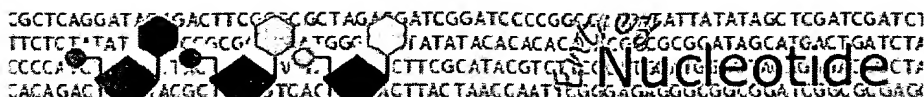


# EXHIBIT A

## CLUSTAL W (1.7) Multiple Sequence Alignments

Sequence format is Pearson  
Sequence 1: PF0148\_3CPA\_SEQIDN01 289 aa  
Sequence 2: gi4583152 282 aa  
Start of Pairwise alignments  
Aligning...  
Sequences (1:2) Aligned. Score: 99  
Start of Multiple Alignment  
There are 1 groups  
Aligning...  
Group 1: Sequences: 2 Score:3912  
Alignment Score 1827  
CLUSTAL-Alignment file created [baaTpaykK.aln]  
CLUSTAL W (1.7) multiple sequence alignment

PF0148_3CPA_SEQIDN01	MSGFSTEERAAPFSLEYRVFLKNEKGQYISPFHDIPIYADKDV FHMVVEVPRWSNAKMEI
gi4583152	----STEERAAAFSLEYRVFLKNEKGQYISPFHDIPIYADKDV FHMVVEVPRWSNAKMEI
	*****
PF0148_3CPA_SEQIDN01	ATKDPLNPIKQDVKKGKRLRYVANLFPYKGYIWNYGAIPTWEDPGHNDKHTGCCGDNDPI
gi4583152	ATKDPLNPIKQDVKKGKRLRYVANLFPYKGYIWNYGAIPTWEDPGHNDKHTGCCGDNDPI
	*****
PF0148_3CPA_SEQIDN01	DVCEIGSKVCARGEIIGVKVLGILAMIDEGETDWKVIAINVDDPDAANYNDINDVKRLKP
gi4583152	DVCEIGSKVCARGEIIGVKVLGILAMIDEGETDWKVIAINVDDPDAANYNDINDVKRLKP
	*****
PF0148_3CPA_SEQIDN01	GYLEATVDWFRRYKVPDGKPFENEFNAEFKDKDFDIDIIKSTHDKWALVTKKTNGKGI
gi4583152	GYLEATVDWFRRYKVPDGKPFENEFNAEFKDKDFDIDIIKSTHDKWALVTKKTNGKGI
	*****
PF0148_3CPA_SEQIDN01	SCMNTTLESFPFKCDPDAARAIVDALPPPCESACTVPTDVKWFHHQKN
gi4583152	SCMNTTLESFPFKCDPDAARAIVDALPPPCESACTVPTDVKWFHH---
	*****



1: AF108211. Homo sapiens cyto...[gi:4583152] [Links](#)

```

1 agcaccgagg agcgcgcggc ggccttctcc ctggagtacc gagtcttcct caaaaatgag
61 aaaggacaat atatatctcc atttcatgat attccaattt atgcagataa ggatgtgttt
121 cacatggtag ttgaagtacc acgctggtct aatgcaaaaa tgggagattgc tacaaaggac
181 cctttaaacc ctattaaaca agatgtgaaa aaaggaaaaac ttgcgtatgt tgcgaatttg

```

241 ttcccgtata aaggatatat ctggaactat ggtgccatcc ctcagacttg ggaagaccca  
301 gggcacaatg ataaacatac tggctgttgt ggtgacaatg acccaattga tgtgtgtgaa  
361 attggaagca aggtatgtgc aagaggtgaa ataattggcg tgaaagttct aggcataattg  
421 gctatgattg acgaagggga aaccgactgg aaagtcattg ccattaatgt ggatgaccc  
481 gatgcagcca attataatga tatcaatgat gtcaaacggc tgaaacctgg ctacttagaa  
541 gctactgtgg actggtttag aagggtataag gttcctgatg gaaaaccaga aaatgagttt  
601 gcgtttaatg cagaatttaa agataaggac tttgccattg atattattaa aagcactcat  
661 gaccattgga aagcattagt gactaagaaa acgaatggaa aaggaatcag ttgcatgaat  
721 acaactttgt ctgagagccc cttcaagtgt gatcctgatg ctgccagagc cattgtggat  
781 gctttaccac caccctgtga atctgcgtgc acagtaccaa cagacgtgga taagtggttc  
841 catcac

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